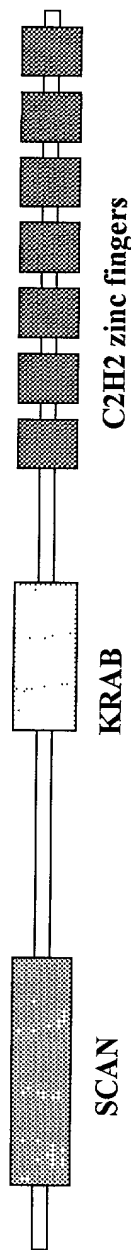


FIG. 1

Structure of MDZ3 and alignment of SCAN box and KRAB motifs

A

MDZ3 (544 a.a.)



B

SCAN box

consensus*.....*.....*.....*.....	60
MDZ3	1 PGPEAFRQRFQRYQE---ASGPREALSRLRELCHQWLRPEVHTKEQILELLVLEQFLT	57
gi 11136033	36 PSPETFLRLFRQRYQE---AAGPQEAALRGQLCRRWLRPELHTKEQILELLVLEQFLT	92
gi 6226799	36 SVWETSHLHFRQLRYHE---TSGPQEAALSRRLRELCHQWLRPEARTKAQILELLVLEQFLS	92
gi 3046745	35 PSPEASHLRRFRFRQE---AAGPQEAALSRRLRELCHQWLRPEMRTKEQILELLVLEQFLT	91
gi 3006231	47 RGPERSRQRFGRFRYPE---AAGPQEAALSRRLRELCHQWLRPEMHSKEQILELLVLEQFLT	103
gi 1731420	49 PDPEIFRQRFRRFCYQN---TFGPREALSRLKELCHQWLRPEINTKEQILELLVLEQFLS	105
gi 11136100	43 LKQELCRQLFRQFCYQD---SPGPREALSRLRELCCQWLKPEIHTKEQILELLVLEQFLT	99
gi 2978255	45 LGQEVFLRLFRQLRYQE---TLGPREALIQLRALCHQWLRPDNTKEQILELLVLEQFLT	101
	118 PGLEAARLRFRCRYED---AIGPQEAALQRELCHQWLRPEVHSKEQVLELLVLEQFLG	174

consensus*.....*.....*.....	90
MDZ3	58 ILPGEIQAWVQEHHPESGEEAVTLVEDLERELDGPRQQV	96
gi 11136033	93 ILPREFYAWIREHGPESGKALAAAMVEDLteraleakvp	131
gi 6226799	93 ILPGEIRTWVQLHHPGSGEEAVALVEELQKDLDPALQV	131
gi 3046745	92 ILPQEIQSRVQELHPESGEEAVTLVEGMQRELGRRLRQQV	130
gi 3006231	104 ILPGNLQSWVREQHPESGEEVVLLLEYLERQLDEPAPQV	142
gi 1731420	106 ILPKELQVWLQEYRPDSGEEAVTLLEDLE--LDLSGQQV	142
gi 11136100	100 ILPGDLQAWVHEHYPSGEEAVTILEDLERGTDEAVLQV	138
gi 2978255	102 ILPEELQTLVKDQLENQEEVVTLLEDLERQIDILGRPV	140
	175 ALPPEIQAVQVGQWPGSPPEAAALVDRRLRWELDGPRKWV	213

FIG. 1

FIG. 1

MDZ3 gene (chr. 7q22.1)

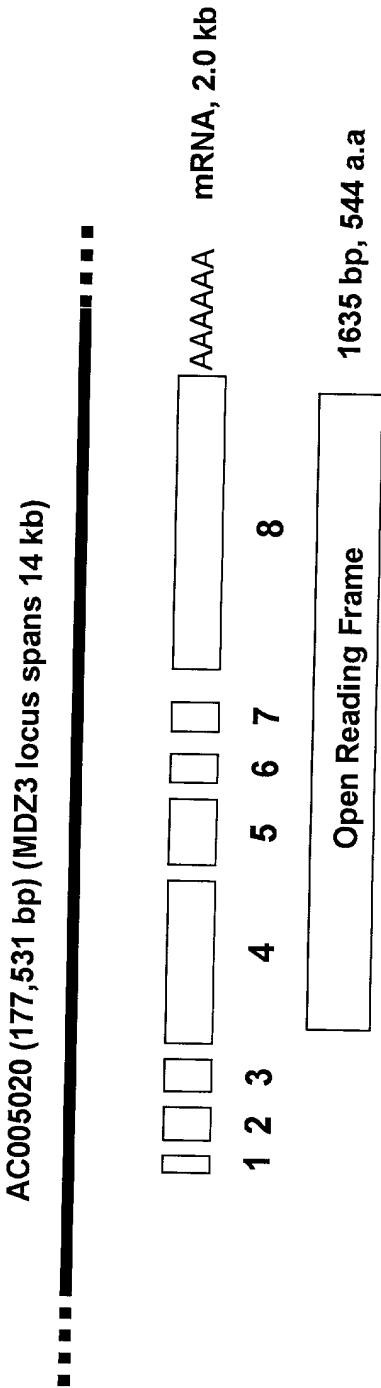


FIG. 2

MDZ3

nt: SEQ ID NO: 1
aa: SEQ ID NO: 3

1 c gga tag cac tgg cga ccc tag cgg gtg aga ggc cct
38 tca ggg ccg cgg cgg gtt gag cgc acc atc aca tct aag
77 cca tca gca agt ttg ttg gtt tta atc tcc aaa ata cgt
116 ctt gat ttt gtc tga ctc ttt gcc acc acc ctg atc taa
155 gcc ctt atc atc tgc ttg aat cac taa ctt gtc tcc act
194 tgc agt ttt taa aag agt tgc ttc cat ttg act ttt tct
233 gtc tgc tgt acc aac ata tga gtt tca gga ggg gtc att
272 gat gca gtc att ctc agt ctc ctc gga ggg agt ctg aag
311 M L K E H P E M A E A P Q
ATG CTT AAA GAG CAT CCA GAG ATG GCG GAA GCT CCT CAG
350 Q Q L G I P V V K L E K E
CAG CAG TTG GGT ATT CCT GTG GTG AAA CTG GAG AAA GAG
389 L P W G R G R E D P S P E
TTG CCA TGG GGC AGA GGA AGG GAG GAC CCT AGT CCA GAG
428 T F R L R F R Q F R Y Q E
ACT TTT CGG CTG AGG TTT CGG CAG TTC CGC TAC CAG GAG
467 A A G P Q E A L R G L Q E
GCA GCT GGA CCC CAG GAA GCT CTT AGG GGG CTC CAG GAG
506 L C R R W L R P E L H T K
CTC TGT CGT CGG TGG CTG AGG CCC GAG TTG CAC ACC AAG
545 E Q I L E L L V L E Q F L
GAG CAG ATC CTG GAG CTG CTG GTG CTG GAG CAG TTC CTC
584 T I L P R E F Y A W I R E
ACT ATC CTG CCC CGC GAG TTC TAC GCC TGG ATC CGG GAG
623 H G P E S G K A L A A M V
CAT GGC CCA GAG AGT GGC AAG GCC CTG GCC GCC ATG GTG

FIG. 3

662	E	D	L	T	E	R	A	L	E	A	K	A	V
	GAG	GAC	CTG	ACA	GAA	AGA	GCA	CTG	GAG	GCC	AAG	GCG	GTT
701	P	C	H	R	Q	G	E	Q	E	E	T	A	L
	CCA	TGC	CAC	AGG	CAG	GGA	GAG	CAG	GAG	GAA	ACA	GCA	CTT
740	C	R	G	A	W	E	P	G	I	Q	L	G	P
	TGC	AGA	GGC	GCT	TGG	GAG	CCA	GGC	ATC	CAG	CTG	GGG	CCA
779	V	E	V	K	P	E	W	G	M	P	P	G	E
	GTG	GAG	GTT	AAG	CCT	GAA	TGG	GGG	ATG	CCC	CCT	GGG	GAA
818	G	V	Q	G	P	D	P	G	T	E	E	Q	L
	GGA	GTT	CAA	GGT	CCA	GAC	CCA	GGT	ACC	GAG	GAG	CAG	CTC
857	S	Q	D	P	G	D	E	T	R	A	F	Q	E
	AGT	CAG	GAC	CCT	GGA	GAT	GAG	ACA	CGG	GCC	TTC	CAG	GAG
896	Q	A	L	P	V	L	Q	A	G	P	G	L	P
	CAA	GCA	CTA	CCT	GTT	CTG	CAG	GCG	GGT	CCT	GGC	CTC	CCC
935	A	V	N	P	R	D	Q	E	M	A	A	G	F
	GCA	GTG	AAT	CCC	AGA	GAC	CAA	GAG	ATG	GCA	GCT	GGG	TTC
974	F	T	A	G	S	Q	G	L	G	P	F	K	D
	TTT	ACT	GCT	GGA	TCG	CAG	GGG	TTG	GGG	CCA	TTT	AAA	GAT
1013	M	A	L	A	F	P	E	E	E	W	R	H	V
	ATG	GCC	CTG	GCC	TTC	CCT	GAG	GAG	GAG	TGG	AGG	CAT	GTG
1052	T	P	A	Q	I	D	C	F	G	E	Y	V	E
	ACC	CCA	GCC	CAG	ATA	GAC	TGC	TTT	GGG	GAG	TAT	GTG	GAA
1091	P	Q	D	C	R	V	S	P	G	G	G	S	K
	CCG	CAG	GAC	TGC	AGG	GTC	TCT	CCA	GGC	GGT	GGG	AGC	AAG
1130	E	K	E	A	K	P	P	Q	E	D	L	K	G
	GAA	AAG	GAG	GCA	AAA	CCC	CCA	CAG	GAA	GAC	CTG	AAA	GGG
1169	A	L	V	A	L	T	S	E	R	F	G	E	A
	GCG	CTG	GTG	GCA	CTG	ACA	TCA	GAG	AGG	TTT	GGG	GAA	GCC
1208	S	L	Q	G	P	G	L	G	R	V	C	E	Q
	TCT	CTC	CAG	GGC	CCT	GGG	CTC	GGA	AGG	GTC	TGT	GAG	CAG
1247	E	P	G	G	P	A	G	S	A	P	G	L	P
	GAG	CCT	GGT	GGC	CCT	GCA	GGC	AGT	GCG	CCT	GGG	CTT	CCT

FIG. 3

0922181-080001

	P	P	Q	H	G	A	I	P	L	P	D	E	V
1286	CCT	CCC	CAG	CAC	GGT	GCC	ATC	CCC	CTG	CCT	GAC	GAA	GTC
	K	T	H	S	S	F	W	K	P	F	Q	C	P
1325	AAA	ACC	CAC	AGC	TCC	TTC	TGG	AAG	CCT	TTC	CAG	TGC	CCT
	E	C	G	K	G	F	S	R	S	S	N	L	V
1364	GAG	TGT	GGG	AAA	GGA	TTC	AGT	CGG	AGC	TCC	AAT	CTC	GTC
	R	H	Q	R	T	H	E	E	K	S	Y	G	C
1403	AGG	CAC	CAG	CGA	ACC	CAC	GAA	GAG	AAG	TCT	TAT	GGC	TGT
	V	E	C	G	K	G	F	T	L	R	E	Y	L
1442	GTG	GAG	TGT	GGG	AAG	GGC	TTT	ACC	CTG	AGA	GAG	TAC	CTG
	M	K	H	Q	R	T	H	L	G	K	R	P	Y
1481	ATG	AAG	CAC	CAG	AGA	ACC	CAC	CTG	GGA	AAG	AGG	CCC	TAC
	V	C	S	E	C	W	K	T	F	S	Q	R	H
1520	GTG	TGC	AGC	GAG	TGC	TGG	AAA	ACC	TTC	AGC	CAG	AGA	CAC
	H	L	E	V	H	Q	R	S	H	T	G	E	K
1559	CAC	CTG	GAG	GTG	CAC	CAG	CGC	AGC	CAC	ACT	GGG	GAG	AAG
	P	H	K	C	G	D	C	W	K	S	F	S	R
1598	CCC	CAC	AAG	TGC	GGG	GAC	TGC	TGG	AAG	AGC	TTC	AGC	CGC
	R	Q	H	L	Q	V	H	R	R	T	H	T	G
1637	AGG	CAG	CAC	CTG	CAG	GTG	CAC	CGG	AGG	ACG	CAC	ACC	GGG
	E	K	P	Y	T	C	E	C	G	K	S	F	S
1676	GAG	AAG	CCC	TAC	ACC	TGC	GAG	TGT	GGC	AAG	AGC	TTC	AGC
	R	N	A	N	L	A	V	H	R	R	A	H	T
1715	AGG	AAT	GCC	AAT	CTG	GCG	GTG	CAC	CGG	CGT	GCC	CAC	ACT
	G	E	K	P	Y	G	C	Q	V	C	G	K	R
1754	GGC	GAG	AAG	CCA	TAT	GGG	TGC	CAG	GTG	TGC	GGG	AAG	CGG
	F	S	K	G	E	R	L	V	R	H	Q	R	I
1793	TTC	AGC	AAA	GGG	GAG	CGG	CTG	GTC	CGA	CAC	CAG	AGA	ATC
	H	T	G	E	K	P	Y	H	C	P	A	C	G
1832	CAT	ACA	GGG	GAG	AAG	CCC	TAC	CAC	TGT	CCT	GCC	TGC	GGG
	R	S	F	N	Q	R	S	I	L	N	R	H	Q
1871	CGA	AGC	TTC	AAC	CAG	AGG	TCC	ATC	CTC	AAC	CGG	CAC	CAG

FIG. 3

	K	T	Q	H	R	Q	E	P	L	V	Q	*
1910	AAG	ACC	CAG	CAC	CGC	CAG	GAG	CCG	CTG	GTG	CAG	TGA gca
1949	tag	cag	gtg	gca	ggc	agc	acc	atc	att	cat	ctt	cgg ata
1988	gca	ctg	gcg	acc	cta	gcg	ggt	gag	agg	ccc	ttc	agg gcc
2027	gcg	gcg	ggt	tga	gcg	cac	cat	cac	atc	taa	gcc	atc agc
2066	aag	ttt	gtt	ggt	ttt	aat	ctc	caa	aat	acg	tct	tga ttt
2105	tgt	ctg	act	ctt	tgc	cac	cac	cct	gat	cta	agc	cct tat
2144	cat	ctg	ctt	gaa	tca	cta	act	tgt	ctc	cac	ttg	cag ttt
2183	tta	aaa	gag	ttg	ctt	cca	ttt	gac	ttt	ttc	tgt	ctg ctg
2222	tac	caa	cat	atg	agt	ttc	agg	agg	ggt	cat	tga	tgc agt
2261	cat	tct	cag	tct	cct	cgg	agg	gag	tct	gaa	gat	gct taa
2300	aga	gca	tcc	aga	gat	ggc	gga	agc	tcc	tca	gca	gca gtt
2339	ggg	tat	tcc	tgt	ggt	gaa	act	gga	gaa	aga	gtt	gcc atg
2378	ggg	cag	agg	aag	gga	gga	ccc	tag	tcc	aga	gac	ttt tcg
2417	gct	gag	gtt	tcg	gca	gtt	ccg	cta	cca	gga	ggc	agc tgg
2456	acc	cca	gga	agc	tct	tag	ggg	gct	cca	gga	gct	ctg tcg
2495	tcg	gtg	gct	gag	gcc	cga	gtt	gca	cac	caa	gga	gca gat
2534	cct	gga	gct	gct	ggt	gct	gga	gca	gtt	cct	cac	tat cct
2573	gcc	ccg	cga	gtt	cta	cgc	ctg	gat	ccg	gga	gca	tgg ccc
2612	aga	gag	tgg	caa	ggc	cct	ggc	cgc	cat	ggt	gga	gga cct
2651	gac	aga	aag	agc	act	gga	ggc	caa	ggc	ggt	tcc	atg cca
2690	cag	gca	ggg	aga	gca	gga	gga	aac	agc	act	ttg	cag agg
2729	cgc	ttg	gga	gcc	agg	cat	cca	gct	ggg	gcc	agt	gga ggt
2768	taa	gcc	tga	atg	ggg	gat	gcc	ccc	tgg	gga	agg	agt tca
2807	agg	tcc	aga	ccc	agg	tac	cga	gga	gca	gct	cag	tca gga
2846	ccc	tgg	aga	tga	gac	acg	ggc	ctt	cca	gga	gca	agc act

FIG. 3

2885 acc tgt tct gca ggc ggg tcc tgg cct ccc cgc agt gaa
 2924 tcc cag aga cca aga gat ggc agc tgg gtt ctt tac tgc
 2963 tgg atc gca ggg gtt ggg gcc att taa aga tat ggc cct
 3002 ggc ctt ccc tga gga gga gtg gag gca tgt gac ccc agc
 3041 cca gat aga ctg ctt tgg gga gta tgt gga acc gca gga
 3080 ctg cag ggt ctc tcc agg cgg tgg gag caa gga aaa gga
 3119 ggc aaa acc ccc aca gga aga cct gaa agg ggc gct ggt
 3158 ggc act gac atc aga gag gtt tgg gga agc ctc tct cca
 3197 ggg ccc tgg gct cgg aag ggt ctg tga gca gga gcc tgg
 3236 tgg ccc tgc agg cag tgc gcc tgg gct tcc tcc tcc cca
 3275 gca cgg tgc cat ccc cct gcc tga cga agt caa aac cca
 3314 cag ctc ctt ctg gaa gcc ttt cca gtg ccc tga gtg tgg
 3353 gaa agg att cag tcg gag ctc caa tct cgt cag gca cca
 3392 gcg aac cca cga aga gaa gtc tta tgg ctg tgt gga gtg
 3431 tgg gaa ggg ctt tac cct gag aga gta cct gat gaa gca
 3470 cca gag aac cca cct ggg aaa gag gcc cta cgt gtg cag
 3509 cga gtg ctg gaa aac ctt cag cca gag aca cca cct gga
 3548 ggt gca cca gcg cag cca cac tgg gga gaa gcc cca caa
 3587 gtg cgg gga ctg ctg gaa gag ctt cag ccg cag gca gca
 3626 cct gca ggt gca ccg gag gac gca cac cgg gga gaa gcc
 3665 cta cac ctg cga gtg tgg caa gag ctt cag cag gaa tgc
 3704 caa tct ggc ggt gca ccg gcg tgc cca cac tgg cga gaa
 3743 gcc ata tgg gtg cca ggt gtg cgg gaa gcg gtt cag caa
 3782 agg gga gcg gct ggt ccg aca cca gag aat cca tac agg
 3821 gga gaa gcc cta cca ctg tcc tgc ctg cgg gcg aag ctt
 3860 caa cca gag gtc cat cct caa ccg gca cca gaa gac cca

FIG. 3

0922181-08001

3938 ggc agg cag cac cat cat tca tct t

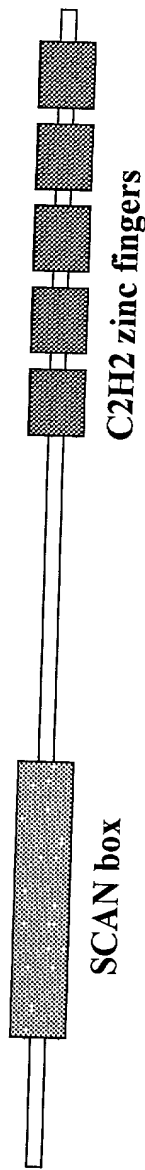
0603

FIG. 3

Structure of MDZ4 and alignment of SCAN box motifs

A

MDZ4 (389 a.a.)



B

SCAN box

consensus	1	PGPEAFRQFRQRYQE	10*	20*	30*	40*	50*	60
MDZ4	42	htrEiFRRRFRQFCYQE	50	-----	60	ASGPREALSRLRELCHQWLRPEVHTKEQI	70	LELLVLEQFLT	80	57			
gi 11136033	36	SVWETSHLHFRQLRYHE	44	-----	54	TSGPQEALSRLRELCHQWLRPEARTKAQI	64	LELLVLEQFLS	74	98			
gi 6226799	35	PSPEASHLRRFRFRFQE	43	-----	53	AAGPREALSRLRELCHQWLRPEMRTKEQI	63	LELLVLEQFLT	73	92			
gi 3046745	47	RGPEERSQRFRGFRYPE	55	-----	65	AAGPREALSRLRELCHQWLRPEMHSKEQI	75	LELLVLEQFLT	85	91			
gi 3006231	49	PDPEIFRQRFRFCYQN	57	-----	67	TFGPREALSRLRELCHQWLRPEINTKEQI	77	LELLVLEQFLS	87	103			
gi 1731420	43	LKQELCRQLFRQFCYQD	51	-----	61	SPGPREALSRLRELCCQWLKPEIHTKEQI	71	LELLVLEQFLT	81	105			
gi 11136100	45	LGQEVFRLRFRQLRYQE	53	-----	63	TLGPREALIQLRALCHQWLRPDINTKEQI	73	LELLVLEQFLT	83	99			
gi 2978255	118	PGLEAARLFRFCFRYED	126	-----	136	AIGPQEALAQRLCHQWLRPEVHSKEQV	146	LELLVLEQFLG	156	174			

consensus	58	ILPGEIQAWVQEHHPESGEEAVTLVEDLERELDGPRQV	66
MDZ4	99	ILPEELQAWVRQHRPVS GEEAVTVLEDLERELDDPGEQV	137
gi 11136033	93	ILPGEIRTWVQLHHPGSGEEAVALVEELQKDLDPGAIQV	131
gi 6226799	92	ILPQEIQSRVQELHPESGEEAVTLVEGMQRELGRLRQV	130
gi 3046745	104	ILPGNLQSWVREQHPSGEEVWVLLLEYLERQLDEPAPQV	142
gi 3006231	106	ILPKELQVWLQYRPDSGEEAVTLLDLE--LDLSGQQV	142
gi 1731420	100	ILPGDLQAWVHEHYPSGEEAVTILEDLERTDEAVLQV	138
gi 11136100	102	ILPEELQTLVKDHQLENGEEVVTLLDRLERQIDILGRP	140
gi 2978255	175	ALPPEIQAVQVQGWPGSPPEAAALVDRLRWELDGPRKWV	213

FIG. 4

The MDZ4 gene (chr. 6p21.3-22.2)

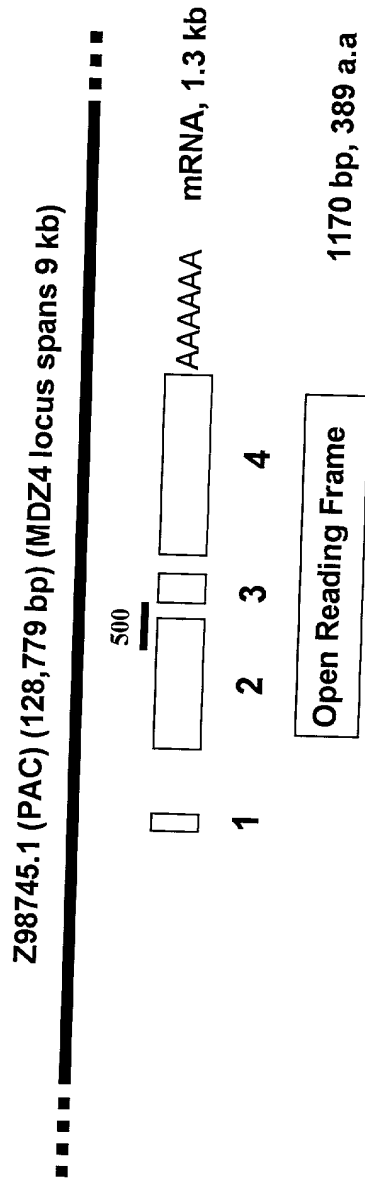


FIG. 5

MDZ4

nt: SEQ ID NO: 3027

aa: SEQ ID NO: 3029

1 gtt gtc aag gat tca gag cag atg tga tct gcg cta ggt
 40 ggc atc tcc tct cac gga tgc ctc gat ctc ggg gtt tcc
 79 aga aga aaa gat caa ggg aga att atc aag aat aga tta
 118 ttt ttc tga ata gtt aaa cct ttg M A I T L
 157 ACC CTT CAG ACT GCA GAG ATG CAG GAA GGA CTT CTG GCA
 196 GTG AAG GTA AAG GAG GAA GAG GAG GAA CAT TCC TGT GGG
 235 CCA GAA TCA GGC CTG TCA AGA AAT AAC CCT CAT ACC AGA
 274 GAG ATC TTT CGT AGA CGC TTC AGG CAG TTC TGC TAT CAG
 313 GAG TCC CCT GGG CCC CGG GAG GCT CTT CAA AGA CTC CAG
 352 GAG CTC TGC CAT CAG TGG CTG AGA CCA GAG ATG CAC ACC
 391 AAG GAG CAG ATC CTA GAG CTG CTG GTG CTG GAG CAG TTC
 430 CTG ACT ATC CTG CCT GAG GAG CTC CAG GCC TGG GTC AGA
 469 CAG CAC CGT CCT GTG AGT GGA GAG GAG GCA GTG ACT GTG
 508 CTG GAG GAT TTG GAG AGA GAG CTG GAT GAC CCA GGA GAG

FIG. 6

00923181-000201

Q V L S H A H E Q E E F V
 547 CAG GTC CTG AGC CAT GCT CAT GAA CAG GAA GAG TTT GTA

K E K A T P G A A Q E S S
 586 AAG GAG AAG GCA ACT CCA GGA GCA GCT CAG GAG TCA TCA

N D Q F Q T L E E Q L G Y
 625 AAT GAC CAA TTC CAA ACC TTG GAA GAG CAG CTT GGG TAT

N L R E V C P V Q E I D G
 664 AAT TTG CGA GAG GTG TGC CCA GTT CAA GAG ATT GAT GGC

K A G T W N V E L A P K R
 703 AAG GCT GGG ACT TGG AAT GTG GAG TTA GCC CCA AAG AGG

E I S Q E V K S L I Q V L
 742 GAG ATT TCT CAG GAA GTG AAA TCT CTT ATA CAA GTT CTT

G K Q N G N I T Q I P E Y
 781 GGA AAA CAG AAT GGT AAT ATT ACT CAG ATT CCT GAG TAT

G D T C D R E G R L E K Q
 820 GGA GAT ACC TGT GAC CGT GAG GGC AGA TTG GAA AAG CAA

R V S S S V E R P Y I C S
 859 AGG GTG AGC TCT TCA GTG GAG AGA CCC TAT ATC TGT AGT

E C G K S F T Q N S I L I
 898 GAA TGT GGA AAA AGC TTC ACC CAG AAT TCC ATC CTT ATC

E H Q R T H T G E K P Y E
 937 GAG CAC CAG AGA ACA CAC ACA GGT GAG AAG CCT TAT GAA

C D E C G R A F S Q R S G
 976 TGT GAT GAG TGT GGG CGG GCC TTC AGC CAG AGG TCA GGC

L F Q H Q R L H T G E K R
 1015 CTA TTC CAG CAC CAG AGA CTC CAC ACT GGG GAG AAG CGC

Y Q C S V C G K A F S Q N
 1054 TAC CAG TGC AGT GTT TGT GGC AAA GCC TTC AGC CAG AAT

A G L F H H L R I H T G E
 1093 GCC GGG CTT TTC CAT CAC CTC AGA ATT CAC ACT GGG GAG

FIG. 6

```

      K   P   Y   Q   C   N   Q   C   N   K   S   F   S
1132 AAG CCT TAC CAG TGC AAT CAG TGC AAT AAG AGT TTT AGT

      R   R   S   V   L   I   K   H   Q   R   I   H   T
1171 CGA CGT TCA GTC CTC ATT AAG CAT CAG AGA ATT CAC ACT

      G   E   R   P   Y   E   C   E   E   C   G   K   N
1210 GGA GAG AGA CCT TAT GAA TGT GAA GAA TGT GGC AAG AAC

      F   I   Y   H   C   N   L   I   Q   H   R   K   V
1249 TTC ATT TAC CAT TGC AAC CTA ATC CAG CAT CGG AAA GTC

      H   P   V   A   E   S   S   *
1288 CAC CCA GTG GCT GAA TCA AGC TAG ctc ctt gga aca ggt

1327 agg
  
```

FIG. 6

T022080" T8T22560

T02080" T022660

Structure of MDZ7

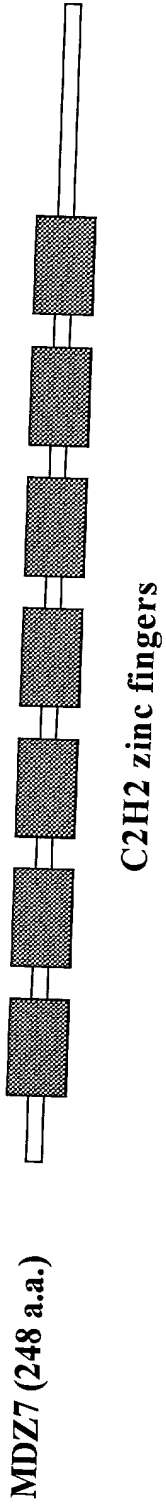


FIG. 7

MDZ7 gene (chr. 16p11.2)

AC002310.1 (BAC) (120,955 bp) (MDZ7 locus spans 5.5 kb)

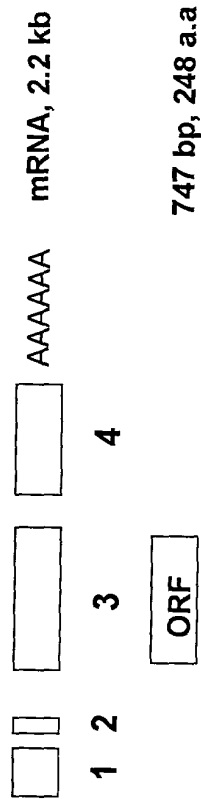


FIG. 8

MDZ7

nt: SEQ ID NO: 4407

aa: SEQ ID NO: 4409

1 cc tgt tcc cgc tgc ccc tcg ggc tgg cac tgc cag gag
39 tac tca gag ctc aaa gct ggg atc tgc agt ccc tta ccc
78 act cag tgc acg ccg cct aag gct ttg cgc ttc acc ttt
117 act cac ctc gaa gcc ctg gac atc cgc atc tgc cct aag
156 act tct cac ctc agt agc aga agg aag tcg cgt cag ctg
195 gcc aca gcc tct ctc cta gga gac cgt ccg gga aaa ggc
234 agt cag ggt aga ccc tga ggc ccc tca gct ccg gct att
273 ttc aga tct gtc gct cct tca ccc tca gcc ttt caa aca
312 ggc cac tcc aaa aaa aag ccc aat cac agc ctt cct tct
351 tct cct ggc ctt ccg gca ctg tcc aat caa cgt acg cca
390 tct atc gga ttt tca gtt ccc aaa ccc gct ttt atc tcg
429 tgg gtg gaa gga gaa gtg gag gcg tgg agc ccg gag gcc
468 cag gat ccc gac ggt gag agc tct gca gct ttc agc agg
507 ggc caa gga cag gaa gca gga tcc agg gat ggg aat gag
546 aag aag gaa agg ctg aag aag tgt cca aaa caa aaa gag
585 gtg gcg cat gaa gtg gct gtc aag gag tgg tgg ccc agc
624 gtc gcc tgc cca gag ttc tgc aac cct agg cag agc ccc
M N P W L K D T L T R R L
663 ATG AAT CCC TGG CTC AAG GAC ACT CTG ACC CGA AGA CTG
P H S C P D C G R N F S Y
703 CCC CAC TCT TGC CCA GAC TGT GGC CGC AAC TTC AGC TAC
P S L L A S H Q R V H S G
742 CCT TCC CTC CTG GCC AGC CAC CAG CGG GTC CAC TCC GGG

FIG. 9

781 E R P F S C G Q C Q A R F
 GAG CGG CCC TTC TCC TGC GGC CAG TGT CAG GCG CGT TTC

820 S Q R R Y L L Q H Q F I H
 TCC CAG CGC AGG TAC CTG CTC CAG CAT CAG TTC ATC CAC

859 T G E K P Y P C P D C G R
 ACC GGC GAG AAG CCC TAC CCC TGC CCC GAC TGC GGG CGC

898 R F R Q R G S L A I H R R
 CGC TTC CGC CAG AGG GGT TCC CTG GCT ATC CAC AGG CGG

937 A H T G E K P Y A C S D C
 GCT CAC ACC GGG GAG AAG CCT TAC GCG TGC TCA GAC TGC

976 K S R F T Y P Y L L A I H
 AAG AGT CGC TTC ACT TAC CCC TAC CTG CTG GCC ATC CAC

1015 Q R K H T G E K P Y S C P
 CAG CGC AAG CAC ACG GGC GAG AAG CCC TAC AGC TGC CCC

1054 D C S L R F A Y T S L L A
 GAT TGC AGC CTC CGT TTC GCC TAC ACC TCC CTG CTG GCC

1093 I H R R I H T G E K P Y P
 ATC CAC AGG CGC ATA CAC ACC GGC GAG AAG CCC TAC CCC

1132 C P D C G R R F T Y S S L
 TGT CCT GAC TGC GGC CGC CGC TTC ACC TAT TCT TCC CTC

1171 L L S H R R I H S D S R P
 CTC CTC AGT CAC CGG CGC ATT CAC TCC GAC AGC CGG CCC

1210 F P C V E C G K G F K R K
 TTC CCC TGC GTG GAG TGT GGG AAA GGC TTC AAG CGC AAG

1249 T A L E A H R W I H R S C
 ACC GCC CTG GAA GCC CAT CGG TGG ATC CAC CGC TCC TGC

1288 S E R R A W Q Q A V V G R
 AGC GAG AGG CGC GCG TGG CAG CAG GCC GTG GTG GGG CGT

1327 S E P I P V L G G K D P P
 TCA GAG CCC ATC CCT GTT TTG GGA GGC AAG GAT CCC CCA

1366 V H F R H F P D I F Q E C
 GTT CAC TTC CGG CAC TTT CCA GAT ATA TTT CAA GAG TGT

G *
 1405 GGG TGA tgg cgt tca cac aaa ctg gtc agc gtt tcc ctg

FIG. 9

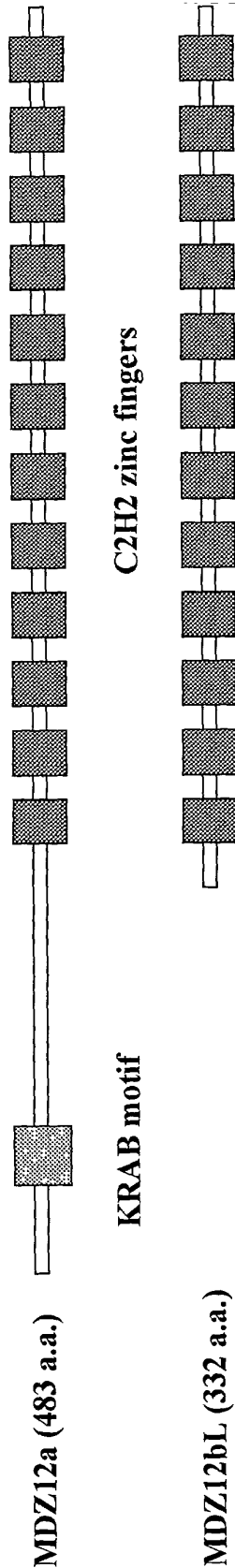
FIG. 9

SECRET



Structure of MDZ12 and alignment of KRAB motifs

A



B

KRAB motif		10	20	30	40	50	60	
consensus	1	VTFFEDVAVYFSQEEWEQLDPAQKNLY-RDVMLENYSNLVSLG-FKVPKPDLSQLEQGEEPWI	61					
MDZ12	1	-----mwlgtsgksglpghclenplqechpaqlleewalkGISRPSVISQPEQKEEPWV	53					
gi 12643434	28	VTFKDVIIVDFTQEEWKQLDPGQDLF-RDVTLENYTHLVSLG-LQVSKPDVISQLEQGTEPWI	88					
gi 141686	1	-----DFTQEEWGQLDPTQRIILY-RDVMLETFGYLLSIG-PELPKPEVISQLEQGTELWV	53					
gi 549835	14	VTFKDVFVDFTREEWKLLDTPAQIIVY-RNVMLENYKNLVSLG-YQLTKPDVILRLEKGEEPWL	74					
gi 3445181	20	VTFGDVAVDFSQEEWEWLNP IQRNLY-RKVMLENYRNLASLG-LCVSKPDVISQLEQGKEPWT	80					
gi 141685	4	VTFGDVAVHFSREEWQCLDPGQRALY-REVMLENHSSVAGLAGFLVFKPELISRLEQGEEPWV	65					
gi 1731444	8	FSFDDLSDVFTQKEWQLLDPSQKNLY-KDVMLENYSSLVSLG-YEVMKPDVIFKLEEGEEPWV	68					
gi 6137309	237	VTFKDVAVCFSDQDWSDDLPTQKEFYgEYVLEEDCGIVVSLsf-PiPRPDEISQV-REEEPWV	297					
gi 3511122	1	MAFEDVAVYFSQEEWGLLDTPAQRIILY-RRVMLDNFALVASLGL-STSRPRVVIQLERGEPEPWV	61					

FIG. 10

Splice Variants of the hMDZ12 Zinc Finger Gene

AC018946 (BAC, 173 kb)

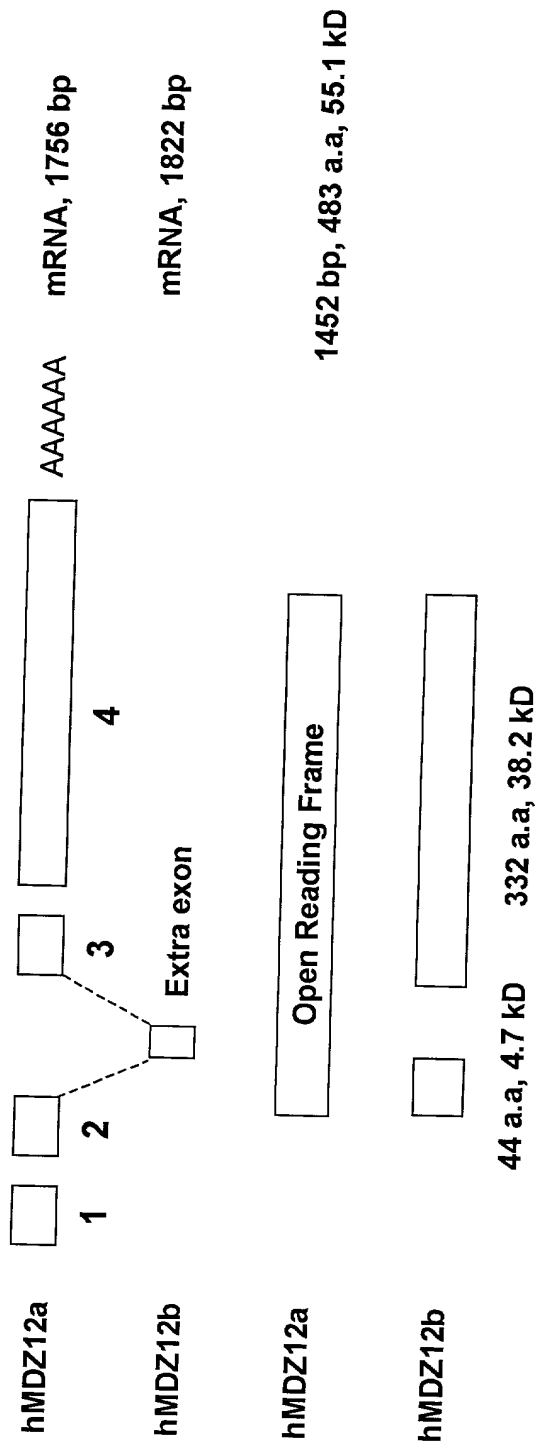


FIG. 11

MDZ12a

nt: SEQ ID NO: 5770

aa: SEQ ID NO: 5772

1 gaa tcc cgg tcg ggt tct ggg agg cac cgc ctc ggg gtt
40 gcg ggc cgg gtg cgg ctc ggc ggt gga gga ctc act tcc
79 tgc tcc atc ccc ggc tgg gcc ctg ggg cgg aac tga tga
118 cgc ttg ata M W L G T S G K S G
157 TTA CCT GGA CAC TGC TTA GAG AAT CCT CTC CAG GAA TGC
196 CAC CCA GCA CAG TTA GAA GAA TGG GCT CTC AAA GGA ATT
235 TCC AGG CCT AGT GTA ATC TCC CAG CCG GAG CAG AAA GAA
274 GAG CCA TGG GTC CTA CCA CTC CAA AAC TTT GAG GCG AGG
313 AAG ATC CCG AGG GAA AGC CAC ACA GAC TGT GAG CAT CAG
352 GTG GCA AAG CTC AAT CAG GAC AAT TCT GAA ACA GCA GAA
391 CAA TGT GGA ACA TCC TCA GAA AGG ACC AAT AAA GAT CTT
430 TCT CAT ACT CTT AGT TGG GGA GGA AAC TGG GAG CAA GGC
469 CTA GAA TTA GAA GGG CAA CAT GGA ACC CTT CCA GGA GAG
508 GGC CAG CTG GAG TCC TTT TCA CAG GAG AGG GAT TTA AAC
547 AAG CTC CTG GAT GGA TAT GTA GGA GAG AAG CCT ATG TGT

FIG. 12

FIG. 12

	A	E	C	G	K	S	F	N	Q	S	S	Y	L
586	GCA	GAA	TGC	GGG	AAA	AGC	TTT	AAC	CAG	AGT	TCC	TAT	CTC
	I	R	H	L	R	T	H	T	G	E	R	P	Y
625	ATA	AGA	CAC	CTA	AGA	ACC	CAC	ACT	GGC	GAG	AGG	CCC	TAT
	T	C	I	E	C	G	K	G	F	K	Q	S	S
664	ACG	TGC	ATT	GAG	TGT	GGG	AAA	GGC	TTC	AAA	CAG	AGC	TCA
	D	L	V	T	H	R	R	T	H	T	G	E	K
703	GAC	CTT	GTC	ACC	CAT	CGC	AGA	ACA	CAC	ACA	GGA	GAG	AAG
	P	Y	Q	C	K	G	C	E	K	K	F	S	D
742	CCC	TAC	CAA	TGC	AAG	GGG	TGT	GAG	AAG	AAA	TTC	AGC	GAC
	S	S	T	L	I	K	H	Q	R	T	H	T	G
781	AGC	TCA	ACA	CTC	ATC	AAA	CAT	CAG	AGA	ACC	CAC	ACA	GGG
	E	R	P	Y	E	C	P	E	C	G	K	T	F
820	GAG	AGA	CCC	TAT	GAG	TGC	CCA	GAG	TGT	GGA	AAG	ACT	TTT
	G	R	K	P	H	L	I	M	H	Q	R	T	H
859	GGG	CGG	AAG	CCA	CAC	CTC	ATA	ATG	CAC	CAA	AGA	ACC	CAC
	T	G	E	K	P	Y	A	C	L	E	C	H	K
898	ACA	GGC	GAG	AAG	CCC	TAC	GCG	TGC	CTG	GAA	TGT	CAC	AAA
	S	F	S	R	S	S	N	F	I	T	H	Q	R
937	AGC	TTC	AGT	CGA	AGC	TCA	AAT	TTC	ATC	ACT	CAC	CAG	AGG
	T	H	T	G	V	K	P	Y	R	C	N	D	C
976	ACC	CAC	ACA	GGG	GTG	AAG	CCT	TAC	AGG	TGT	AAT	GAC	TGT
	G	E	S	F	S	Q	S	S	D	L	I	K	H
1015	GGG	GAG	AGT	TTT	AGC	CAG	AGC	TCG	GAT	TTG	ATT	AAG	CAC
	Q	R	T	H	T	G	E	R	P	F	K	C	P
1054	CAA	CGA	ACC	CAC	ACG	GGA	GAA	CGG	CCC	TTC	AAA	TGC	CCG
	E	C	G	K	G	F	R	D	S	S	H	F	V
1093	GAG	TGC	GGG	AAG	GGC	TTC	AGA	GAT	AGT	TCT	CAT	TTT	GTA
	A	H	M	S	T	H	S	G	E	R	P	F	S
1132	GCT	CAC	ATG	AGC	ACT	CAT	TCA	GGA	GAG	AGG	CCT	TTC	AGT
	C	P	D	C	H	K	S	F	S	Q	S	S	H
1171	TGT	CCT	GAC	TGC	CAC	AAA	AGC	TTC	AGT	CAG	AGC	TCA	CAT
	L	V	T	H	Q	R	T	H	T	G	E	R	P
1210	TTG	GTC	ACG	CAC	CAA	AGA	ACA	CAC	ACA	GGT	GAG	AGA	CCT

FIG. 12

0922181-000001

	F	K	C	E	N	C	G	K	G	F	A	D	S
1249	TTT	AAG	TGC	GAA	AAC	TGT	GGG	AAA	GGA	TTC	GCC	GAC	AGC
	S	A	L	I	K	H	Q	R	I	H	T	G	E
1288	TCC	GCC	CTC	ATT	AAG	CAC	CAA	CGA	ATC	CAC	ACC	GGA	GAA
	R	P	Y	K	C	G	E	C	G	K	S	F	N
1327	AGA	CCC	TAC	AAA	TGT	GGA	GAG	TGT	GGG	AAG	AGC	TTC	AAT
	Q	S	S	H	F	I	T	H	Q	R	I	H	L
1366	CAG	AGC	TCC	CAC	TTT	ATT	ACC	CAT	CAG	CGA	ATC	CAC	TTA
	G	D	R	P	Y	R	C	P	E	C	G	K	T
1405	GGA	GAC	AGG	CCC	TAT	CGA	TGT	CCT	GAG	TGT	GGC	AAG	ACC
	F	N	Q	R	S	H	F	L	T	H	Q	R	T
1444	TTC	AAT	CAG	CGT	TCC	CAT	TTC	CTC	ACA	CAC	CAG	AGA	ACG
	H	T	G	E	K	P	F	H	C	S	K	C	N
1483	CAT	ACA	GGA	GAA	AAA	CCT	TTC	CAC	TGT	AGT	AAA	TGT	AAC
	K	S	F	R	Q	K	A	H	L	L	C	H	Q
1522	AAG	AGC	TTC	CGT	CAG	AAA	GCG	CAT	CTT	TTA	TGC	CAT	CAA
	N	T	H	L	I	*							
1561	AAC	ACC	CAT	TTG	ATT	TAG	gaa	gta	gtc	ttt	ggt	gtt	cag
1600	ctg	ctc	cct	tgc	aca	ttt	tca	ttg	cta	ctg	tct	tca	agc
1639	acc	cca	aat	aga	gaa	aac	ctg	ggc	gtc	agt	ggc	tca	att
1678	tgg	gcc	ctg	atc	tat	tct	ccc	tct	ttc	ttg	tct	atg	tta
1717	taa	cag	aga	gga	taa	act	taa	agg	gtc	caa	ata	acg	gtc
1756	caa	aaa	aaa	aaa	aaa	aaa	aaa	aaa	a				

FIG. 12

MDZ12b

nt: SEQ ID NO: 6938
 aa: SEQ ID NO: 6939 and 6940

M	W	L	G	T	S	G	K	S	G	L	P	G	13
ATG	TGG	CTG	GGG	ACT	TCA	GGG	AAG	AGT	GGG	TTA	CCT	GGA	39
H	C	L	E	N	P	L	Q	E	C	H	P	A	26
CAC	TGC	TTA	GAG	AAT	CCT	CTC	CAG	GAA	TGC	CAC	CCA	GCA	78
Q	L	E	E	W	A	L	K	G	L	G	W	T	39
CAG	TTA	GAA	GAA	TGG	GCT	CTC	AAA	GGA	CTG	GGT	TGG	ACT	117
L	T	S	A	T	*								45
CTC	ACC	TCT	GCC	ACT	TAA	cttctgagacttctgaggtctttgtgg							162
aaaaggagaatttccaggcctagtgtaatctcccagccggagcagaaagaag													214
agccatgggtcctaccactccaaaactttgaggcgaggaagatcccgagggga													266
aagccacacagactgtgagcatcaggtggcaaagctcaatcaggacaattct													318
gaaacagcagaacaatgtggaacatcctcagaaaggaccaataaagatcttt													370
ctcatactcttagttggggaggaaactgggagcaaggcctagaattagaagg													422
gcaacatggaacccttccaggagagggccagctggagtccttttcacaggag													474
										M	C		2
agggattttaacaagctcctggatggatatgtaggagagaagcctATG										TGT			525
A	E	C	G	K	S	F	N	Q	S	S	Y	L	15
GCA	GAA	TGC	GGG	AAA	AGC	TTT	AAC	CAG	AGT	TCC	TAT	CTC	564
I	R	H	L	R	T	H	T	G	E	R	P	Y	28
ATA	AGA	CAC	CTA	AGA	ACC	CAC	ACT	GGC	GAG	AGG	CCC	TAT	603
T	C	I	E	C	G	K	G	F	K	Q	S	S	41
ACG	TGC	ATT	GAG	TGT	GGG	AAA	GGC	TTC	AAA	CAG	AGC	TCA	642
D	L	V	T	H	R	R	T	H	T	G	E	K	54
GAC	CTT	GTC	ACC	CAT	CGC	AGA	ACA	CAC	ACA	GGA	GAG	AAG	681
P	Y	Q	C	K	G	C	E	K	K	F	S	D	67
CCC	TAC	CAA	TGC	AAG	GGG	TGT	GAG	AAG	AAA	TTC	AGC	GAC	720

FIG. 13

S	S	T	L	I	K	H	Q	R	T	H	T	G	80
AGC	TCA	ACA	CTC	ATC	AAA	CAT	CAG	AGA	ACC	CAC	ACA	GGG	759
E	R	P	Y	E	C	P	E	C	G	K	T	F	93
GAG	AGA	CCC	TAT	GAG	TGC	CCA	GAG	TGT	GGA	AAG	ACT	TTT	798
G	R	K	P	H	L	I	M	H	Q	R	T	H	106
GGG	CGG	AAG	CCA	CAC	CTC	ATA	ATG	CAC	CAA	AGA	ACC	CAC	837
T	G	E	K	P	Y	A	C	L	E	C	H	K	119
ACA	GGC	GAG	AAG	CCC	TAC	GCG	TGC	CTG	GAA	TGT	CAC	AAA	876
S	F	S	R	S	S	N	F	I	T	H	Q	R	132
AGC	TTC	AGT	CGA	AGC	TCA	AAT	TTC	ATC	ACT	CAC	CAG	AGG	915
T	H	T	G	V	K	P	Y	R	C	N	D	C	145
ACC	CAC	ACA	GGG	GTG	AAG	CCT	TAC	AGG	TGT	AAT	GAC	TGT	954
G	E	S	F	S	Q	S	S	D	L	I	K	H	158
GGG	GAG	AGT	TTT	AGC	CAG	AGC	TCG	GAT	TTG	ATT	AAG	CAC	993
Q	R	T	H	T	G	E	R	P	F	K	C	P	171
CAA	CGA	ACC	CAC	ACG	GGA	GAA	CGG	CCC	TTC	AAA	TGC	CCG	1032
E	C	G	K	G	F	R	D	S	S	H	F	V	184
GAG	TGC	GGG	AAG	GGC	TTC	AGA	GAT	AGT	TCT	CAT	TTT	GTA	1071
A	H	M	S	T	H	S	G	E	R	P	F	S	197
GCT	CAC	ATG	AGC	ACT	CAT	TCA	GGA	GAG	AGG	CCT	TTC	AGT	1110
C	P	D	C	H	K	S	F	S	Q	S	S	H	210
TGT	CCT	GAC	TGC	CAC	AAA	AGC	TTC	AGT	CAG	AGC	TCA	CAT	1149
L	V	T	H	Q	R	T	H	T	G	E	R	P	223
TTG	GTC	ACG	CAC	CAA	AGA	ACA	CAC	ACA	GGT	GAG	AGA	CCT	1188
F	K	C	E	N	C	G	K	G	F	A	D	S	236
TTT	AAG	TGC	GAA	AAC	TGT	GGG	AAA	GGA	TTC	GCC	GAC	AGC	1227
S	A	L	I	K	H	Q	R	I	H	T	G	E	249
TCC	GCC	CTC	ATT	AAG	CAC	CAA	CGA	ATC	CAC	ACC	GGA	GAA	1266
R	P	Y	K	C	G	E	C	G	K	S	F	N	262
AGA	CCC	TAC	AAA	TGT	GGA	GAG	TGT	GGG	AAG	AGC	TTC	AAT	1305
Q	S	S	H	F	I	T	H	Q	R	I	H	L	275
CAG	AGC	TCC	CAC	TTT	ATT	ACC	CAT	CAG	CGA	ATC	CAC	TTA	1344
G	D	R	P	Y	R	C	P	E	C	G	K	T	288
GGA	GAC	AGG	CCC	TAT	CGA	TGT	CCT	GAG	TGT	GGC	AAG	ACC	1383

FIG. 13

099231.0000

F	N	Q	R	S	H	F	L	T	H	Q	R	T	301
TTC	AAT	CAG	CGT	TCC	CAT	TTC	CTC	ACA	CAC	CAG	AGA	ACG	1422
H	T	G	E	K	P	F	H	C	S	K	C	N	314
CAT	ACA	GGA	GAA	AAA	CCT	TTC	CAC	TGT	AGT	AAA	TGT	AAC	1461
K	S	F	R	Q	K	A	H	L	L	C	H	Q	327
AAG	AGC	TTC	CGT	CAG	AAA	GCG	CAT	CTT	TTA	TGC	CAT	CAA	1500
N	T	H	L	I	*								323
AAC	ACC	CAT	TTG	ATT	TAG								1518

FIG. 13

09221-00201
"TBT250"

MDZ3 Expression: RT-PCR Analysis

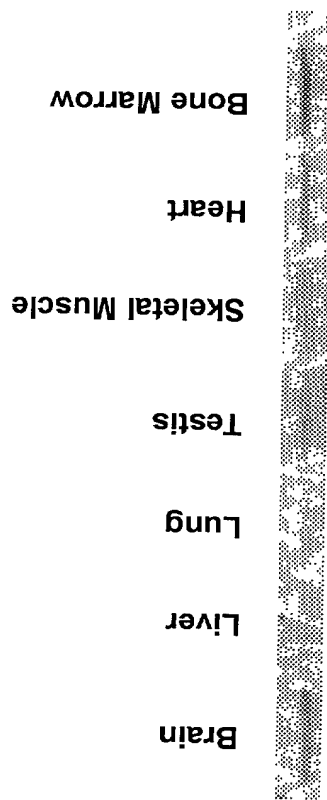


FIG. 14

MDZ7 Expression: RT-PCR Analysis

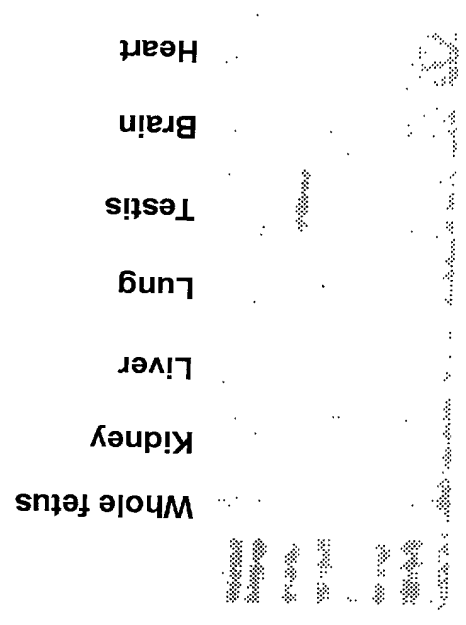


FIG. 15

Expression of MDZ12 in human tissues

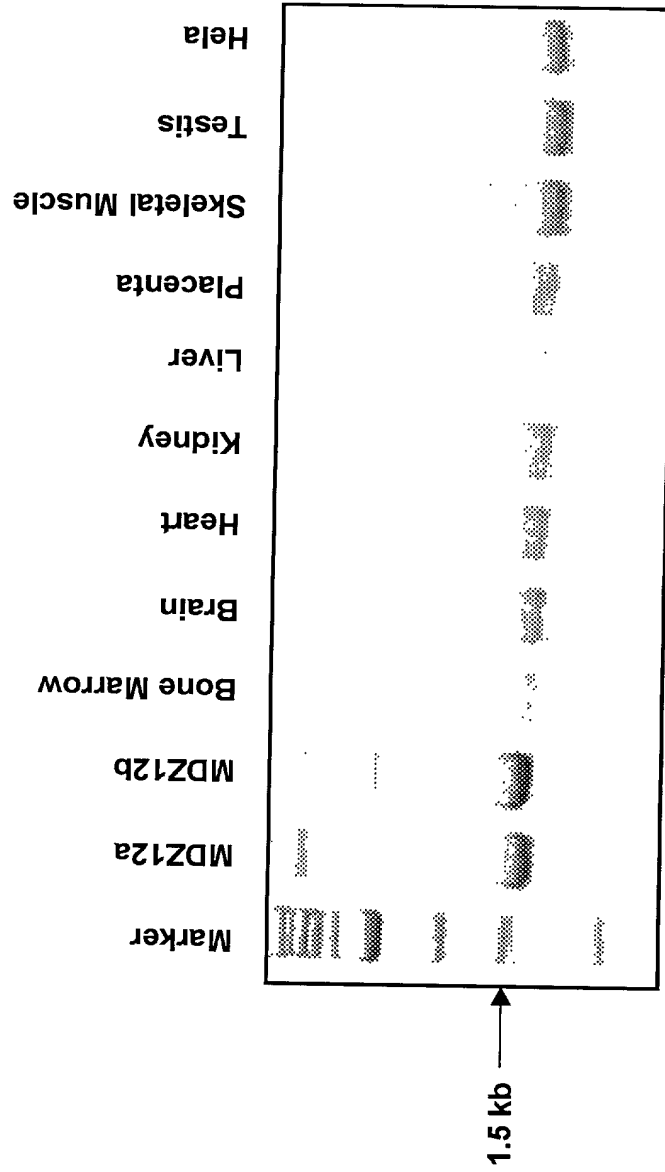


FIG. 16